

SEQUENCE LISTING

<110> Chiaki Senoo
Mariko Numata

<120> Novel Trypsin Family Serine Proteases

<130> 50026/027001

<140> US 09/831,180

<141> 2001-05-03

<150> PCT/JP99/06111

<151> 1999-11-02

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Pro Ala Ser Ala Ile Val Gly Gly Lys Pro Ala Asn Ile Leu Glu Phe
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Pro Trp His Val Gly Ile Met Asn His Gly Ser His Leu Cys Gly Gly
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Val	Cys	Asn	Lys	Lys	Arg	Asn	Thr	Ala	Ile	Trp	Tyr	Gln	Val	Gly	Ile
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Met Met Leu Pro Leu Leu Ile Ala Leu Leu Met Ala Ser Lys
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gga caa gct aag gac cag caa gaa tca gtt ctg tgt ggc cac aga cct 158
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15 20 25

gcc ttc cca aac tca tca tgg ctg cca ttg cgg gag ctg ctt gag gtc 206
Ala Phe Pro Asn Ser Ser Trp Leu Pro Leu Arg Glu Leu Leu Glu Val 45
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cag cat ggt gag ttc cca tgg caa gtg agt atc cag atg ctt ggg aaa 254
Gln His Gly Glu Phe Pro Trp Gln Val Ser Ile Gln Met Leu Gly Lys 60
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cac ctg tgt gga ggc tcc atc atc cac cgg tgg tgg gtt ctg aca gca 302
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Thr Val Val Met Gly Ile Lys Thr Phe Ser Asp Thr Asn Leu Glu Arg 110
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Lys Gln Val Gln Lys Ile Ile Ala His Arg Asp Tyr Lys Pro Pro Asp 125
115 120

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Leu Asp Ser Asp Leu Cys Leu Leu Leu Leu Ala Thr Pro Ile Gln Phe 140
130 135

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Asn Lys Asp Lys Met Pro Ile Cys Leu Pro Gln Arg Glu Asn Ser Trp 155
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Asp Arg Cys Trp Met Ser Glu Trp Ala Tyr Thr His Gly His Gly Ser 170
160 165

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Ala Lys Gly Ser Asn Met His Leu Lys Lys Leu Arg Val Val Gln Ile 190
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Cys																				

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 35 40 45
 Gly Glu Phe Pro Trp Gln Val Ser Ile Gln Met Leu Gly Lys His Leu
 50 55 60
 Cys Gly Gly Ser Ile Ile His Arg Trp Trp Val Leu Thr Ala Ala His
 65 70 75 80
 Cys Phe Pro Arg Thr Leu Leu Glu Leu Val Ala Val Asn Val Thr Val
 85 90 95
 Val Met Gly Ile Lys Thr Phe Ser Asp Thr Asn Leu Glu Arg Lys Gln
 100 105 110
 Val Gln Lys Ile Ile Ala His Arg Asp Tyr Lys Pro Pro Asp Leu Asp
 115 120 125
 Ser Asp Leu Cys Leu Leu Leu Leu Ala Thr Pro Ile Gln Phe Asn Lys
 130 135 140

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Cys	Trp	Met	Ser	Glu	Trp	Ala	Tyr	Thr	His	Gly	His	Gly	Ser	Ala	Lys
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Gly	Ser	Asn	Met	His	Leu	Lys	Lys	Leu	Arg	Val	Val	Gln	Ile	Ser	Trp
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Gln	Arg	Glu	Gly	Arg	Ala	Leu	Ala	Leu	Ser	Lys	Ala	Ser	Lys	Ser	Leu
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 Ala Phe Pro Asn Ser Ser Trp Leu Pro Phe His Glu Arg Leu Gln Val
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Ala His Cys Phe Arg Arg Thr Leu Leu Asp Met Ala Val Val Asn Val	
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Thr Val Val Met Gly Thr Arg Thr Phe Ser Asn Ile His Ser Glu Arg	
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ctc gac agt gac ctc tct ctg ctt cta ctt gcc aca cca gtg caa ttc	495
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Ile Cys Ala Ser Asn Glu Pro Gly Thr Asn Gly Ile Phe Lys Gly Asp	
210 215 220	
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Ser Gly Ala Pro Leu Val Cys Ala Ile Tyr Gly Thr Gln Arg Leu Phe	
225 230 235	
caa gtg ggt gtc ttc agt ggg ggc ata aga tct ggc tcc agg ggg aga	831
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 35 40 45
 Glu Cys Pro Trp Gln Val Ser Ile Gln Met Ser Arg Lys His Leu Cys
 50 55 60
 Gly Gly Ser Ile Leu His Trp Trp Trp Val Leu Thr Ala Ala His Cys
 65 70 75 80
 Phe Arg Arg Thr Leu Leu Asp Met Ala Val Val Asn Val Thr Val Val
 85 90 95
 Met Gly Thr Arg Thr Phe Ser Asn Ile His Ser Glu Arg Lys Gln Val
 100 105 110
 Gln Lys Val Ile Ile His Lys Asp Tyr Lys Pro Pro Gln Leu Asp Ser
 115 120 125
 Asp Leu Ser Leu Leu Leu Leu Ala Thr Pro Val Gln Phe Ser Asn Phe
 130 135 140
 Lys Met Pro Val Cys Leu Gln Glu Glu Glu Arg Thr Trp Asp Trp Cys
 145 150 155 160
 Trp Met Ala Gln Trp Val Thr Thr Asn Gly Tyr Asp Gln Tyr Asp Asp
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 Leu Asn Met His Leu Glu Lys Leu Arg Val Val Gln Ile Ser Arg Lys
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 Glu Cys Ala Lys Arg Val Asn Gln Leu Ser Arg Asn Met Ile Cys Ala
 195 200 205
 Ser Asn Glu Pro Gly Thr Asn Gly Ile Phe Lys Gly Asp Ser Gly Ala
 210 215 220
 Pro Leu Val Cys Ala Ile Tyr Gly Thr Gln Arg Leu Phe Gln Val Gly
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<220>
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25 30 35	
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Gln Glu Ala Glu Leu Gly Glu Phe Pro Trp Gln Val Ser Ile Gln Glu	
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agt gac cac cat ttc tgc ggc ggc tcc att ctc agt gag tgg tgg atc	247
Ser Asp His His Phe Cys Gly Gly Ser Ile Leu Ser Glu Trp Trp Ile	
55 60 65 70	
ctc acc gtg gcc cac tgc ttc tat gct cag gag ctt tcc cca aca gat	295
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75 80 85	
ctc aga gtc aga gtg gga acc aat gac tta act act tca ccc gtg gaa	343
Leu Arg Val Arg Val Gly Thr Asn Asp Leu Thr Thr Ser Pro Val Glu	
90 95 100	
cta gag gtc acc acc ata atc cgg cac aaa ggc ttt aaa cgg ctg aac	391
Leu Glu Val Thr Thr Ile Ile Arg His Lys Gly Phe Lys Arg Leu Asn	
105 110 115	
atg gac aac gac att gcc ttg ttg ctg cta gcc aag ccc ttg gcg ttc	439
Met Asp Asn Asp Ile Ala Leu Leu Leu Leu Ala Lys Pro Leu Ala Phe	
120 125 130	
aat gag ctg acg gtg ccc atc tgc ctt cct ctc tgg ccc gcc cct ccc	487
Asn Glu Leu Thr Val Pro Ile Cys Leu Pro Leu Trp Pro Ala Pro Pro	
135 140 145 150	
agc tgg cac gaa tgc tgg gtg gca gga tgg ggc gta acc aac tca act	535
Ser Trp His Glu Cys Trp Val Ala Gly Trp Gly Val Thr Asn Ser Thr	
155 160 165	
gac aag gaa tct atg tca acg gat ctg atg aag gtg ccc atg cgt atc	583
Asp Lys Glu Ser Met Ser Thr Asp Leu Met Lys Val Pro Met Arg Ile	
170 175 180	
ata gag tgg gag gaa tgc tta cag atg ttt ccc agc ctc acc aca aac	631
Ile Glu Trp Glu Glu Cys Leu Gln Met Phe Pro Ser Leu Thr Thr Asn	
185 190 195	
atg ctg tgt gcc tca tat ggt aat gag agc tac gat gct tgc cag ggt	679
Met Leu Cys Ala Ser Tyr Gly Asn Glu Ser Tyr Asp Ala Cys Gln Gly	
200 205 210	
gac agt ggg gga ccg ctt gtc tgc acc aca gat cct ggc agt agg tgg	727
Asp Ser Gly Gly Pro Leu Val Cys Thr Thr Asp Pro Gly Ser Arg Trp	
215 220 225 230	
tac cag gtg ggc atc atc agc tgg ggc aag agc tgt gga aaa aaa ggc	775
Tyr Gln Val Gly Ile Ile Ser Trp Gly Lys Ser Cys Gly Lys Lys Gly	
235 240 245	
ttc cca ggg ata tat act gta ttg gca aag tat acc ctg tgg att gag	823
Phe Pro Gly Ile Tyr Thr Val Leu Ala Lys Tyr Thr Leu Trp Ile Glu	

250	255	260	
aaa ata gcc cag aca gag ggg aag ccc ctg gat ttt aga ggt cag agc			871
Lys Ile Ala Gln Thr Glu Gly Lys Pro Leu Asp Phe Arg Gly Gln Ser			
265	270	275	
tcc tct aac aag aag aaa aac aga cag aac aat cag ctc tcc aaa tcc			919
Ser Ser Asn Lys Lys Lys Asn Arg Gln Asn Asn Gln Leu Ser Lys Ser			
280	285	290	
cca gcc ctg aac tgc ccc caa agc tgg ctc ctg ccc tgt ctg ctg tcc			967
Pro Ala Leu Asn Cys Pro Gln Ser Trp Leu Leu Pro Cys Leu Leu Ser			
295	300	305	310
ttt gca ctg ctt aga gcc ttg tcc aac tgg aaa taaaacaatg cagtctctga			1020
Phe Ala Leu Leu Arg Ala Leu Ser Asn Trp Lys			
315	320		
tccaccct			1028
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<211> 321			
<212> PRT			
<213> Mus musculus			
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Met Ile Leu Pro Ser Ile Leu Leu Leu Val Ala His Thr Leu Glu Ala			
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Asn Val Glu Cys Gly Val Arg Pro Leu Tyr Asp Ser Arg Ile Gln Tyr			
20 25 30			
Ser Arg Ile Ile Glu Gly Gln Glu Ala Glu Leu Gly Glu Phe Pro Trp			
35 40 45			
Gln Val Ser Ile Gln Glu Ser Asp His His Phe Cys Gly Gly Ser Ile			
50 55 60			
Leu Ser Glu Trp Trp Ile Leu Thr Val Ala His Cys Phe Tyr Ala Gln			
65 70 75 80			
Glu Leu Ser Pro Thr Asp Leu Arg Val Arg Val Gly Thr Asn Asp Leu			
85 90 95			
Thr Thr Ser Pro Val Glu Leu Glu Val Thr Thr Ile Ile Arg His Lys			
100 105 110			
Gly Phe Lys Arg Leu Asn Met Asp Asn Asp Ile Ala Leu Leu Leu Leu			
115 120 125			
Ala Lys Pro Leu Ala Phe Asn Glu Leu Thr Val Pro Ile Cys Leu Pro			
130 135 140			
Leu Trp Pro Ala Pro Pro Ser Trp His Glu Cys Trp Val Ala Gly Trp			
145 150 155 160			
Gly Val Thr Asn Ser Thr Asp Lys Glu Ser Met Ser Thr Asp Leu Met			
165 170 175			
Lys Val Pro Met Arg Ile Ile Glu Trp Glu Glu Cys Leu Gln Met Phe			
180 185 190			
Pro Ser Leu Thr Thr Asn Met Leu Cys Ala Ser Tyr Gly Asn Glu Ser			
195 200 205			
Tyr Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Thr Thr			
210 215 220			
Asp Pro Gly Ser Arg Trp Tyr Gln Val Gly Ile Ile Ser Trp Gly Lys			
225 230 235 240			
Ser Cys Gly Lys Lys Gly Phe Pro Gly Ile Tyr Thr Val Leu Ala Lys			
245 250 255			
Tyr Thr Leu Trp Ile Glu Lys Ile Ala Gln Thr Glu Gly Lys Pro Leu			

			260					265				270							
Asp	Phe	Arg	Gly	Gln	Ser	Ser	Ser	Asn	Lys	Lys	Lys	Asn	Arg	Gln	Asn				
		275						280				285							
Asn	Gln	Leu	Ser	Lys	Ser	Pro	Ala	Leu	Asn	Cys	Pro	Gln	Ser	Trp	Leu				
	290					295					300								
Leu	Pro	Cys	Leu	Leu	Ser	Phe	Ala	Leu	Leu	Arg	Ala	Leu	Ser	Asn	Trp				
305					310					315					320				
Lys																			

<210> 9
 <211> 1123
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (41)...(1096)

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																	Met Leu Leu Phe Ser
																	1 5
gtg ttg ctg ctc ctg tcc ctg gtc acg gga act cag ctc ggt cca cgg	103																
Val Leu Leu Leu Leu Ser Leu Val Thr Gly Thr Gln Leu Gly Pro Arg																	
	10							15						20			
act cct ctc cca gag gct gga gtg gct atc cta ggc agg gct agg gga	151																
Thr Pro Leu Pro Glu Ala Gly Val Ala Ile Leu Gly Arg Ala Arg Gly																	
	25						30					35					
gcc cac cgc cct cag ccc cgt cat ccc ccc agc cca gtc agt gaa tgt	199																
Ala His Arg Pro Gln Pro Arg His Pro Pro Ser Pro Val Ser Glu Cys																	
	40						45					50					
ggg gac aga tct att ttc gag gga aga act cgg tat tcc aga atc aca	247																
Gly Asp Arg Ser Ile Phe Glu Gly Arg Thr Arg Tyr Ser Arg Ile Thr																	
	55					60				65							
ggg ggg atg gag gcg gag gtg ggt gag ttt ccg tgg cag gtg agt att	295																
Gly Gly Met Glu Ala Glu Val Gly Glu Phe Pro Trp Gln Val Ser Ile																	
	70				75			80						85			
cag gca aga agt gaa cct ttc tgt ggc ggc tcc atc ctc aac aag tgg	343																
Gln Ala Arg Ser Glu Pro Phe Cys Gly Gly Ser Ile Leu Asn Lys Trp																	
	90						95						100				
tgg att ctc act gcg gct cac tgc tta tat tcc gag gag ctg ttt cca	391																
Trp Ile Leu Thr Ala Ala His Cys Leu Tyr Ser Glu Glu Leu Phe Pro																	
	105						110					115					
gaa gaa ctg agt gtc gtg ctg ggg acc aac gac tta act agc cca tcc	439																
Glu Glu Leu Ser Val Val Leu Gly Thr Asn Asp Leu Thr Ser Pro Ser																	
	120					125				130							
atg gaa ata aag gag gtc gcc agc atc att ctt cac aaa gac ttt aag	487																
Met Glu Ile Lys Glu Val Ala Ser Ile Ile Leu His Lys Asp Phe Lys																	

135	140	145	
aga gcc aac atg gac aat gac att gcc ttg ctg ctg ctg gct tcg ccc			535
Arg Ala Asn Met Asp Asn Asp Ile Ala Leu Leu Leu Leu Ala Ser Pro			
150	155	160	165
atc aag ctc gat gac ctg aag gtg ccc atc tgc ctc ccc acg cag ccc			583
Ile Lys Leu Asp Asp Leu Lys Val Pro Ile Cys Leu Pro Thr Gln Pro			
	170	175	180
ggc cct gcc aca tgg cgc gaa tgc tgg gtg gca ggt tgg ggc cag acc			631
Gly Pro Ala Thr Trp Arg Glu Cys Trp Val Ala Gly Trp Gly Gln Thr			
	185	190	195
aat gct gct gac aaa aac tct gtg aaa acg gat ctg atg aaa gcg cca			679
Asn Ala Ala Asp Lys Asn Ser Val Lys Thr Asp Leu Met Lys Ala Pro			
	200	205	210
atg gtc atc atg gac tgg gag gag tgt tca aag atg ttt cca aaa ctt			727
Met Val Ile Met Asp Trp Glu Glu Cys Ser Lys Met Phe Pro Lys Leu			
	215	220	225
acc aaa aat atg ctg tgt gcc gga tac aag aat gag agc tat gat gcc			775
Thr Lys Asn Met Leu Cys Ala Gly Tyr Lys Asn Glu Ser Tyr Asp Ala			
	230	235	240
tgc aag ggt gac agt ggg ggg cct ctg gtc tgc acc cca gag cct ggt			823
Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Thr Pro Glu Pro Gly			
	250	255	260
gag aag tgg tac cag gtg ggc atc atc agc tgg gga aag agc tgt gga			871
Glu Lys Trp Tyr Gln Val Gly Ile Ile Ser Trp Gly Lys Ser Cys Gly			
	265	270	275
gat aag aac acc cca ggg ata tac acc tgc ttg gtg aac tac aac ctc			919
Asp Lys Asn Thr Pro Gly Ile Tyr Thr Ser Leu Val Asn Tyr Asn Leu			
	280	285	290
tgg atc gag aaa gtg acc cag cta gga ggc agg ccc ttc aat gca gag			967
Trp Ile Glu Lys Val Thr Gln Leu Gly Gly Arg Pro Phe Asn Ala Glu			
	295	300	305
aaa agg agg act tct gtc aaa cag aaa cct atg ggc tcc cca gtc tcg			1015
Lys Arg Arg Thr Ser Val Lys Gln Lys Pro Met Gly Ser Pro Val Ser			
	310	315	320
gga gtc cca gag cca ggc agc ccc aga tcc tgg ctc ctg ctc tgt ccc			1063
Gly Val Pro Glu Pro Gly Ser Pro Arg Ser Trp Leu Leu Leu Cys Pro			
	330	335	340
ctg tcc cat gtg ttg ttc aga gct att ttg tac tgataataaaa atagaggcta			1116
Leu Ser His Val Leu Phe Arg Ala Ile Leu Tyr			
	345	350	
ttcttttc			1123
<210> 10			
<211> 352			
<212> PRT			

<213> Homo sapiens

<400> 10

Met	Leu	Leu	Phe	Ser	Val	Leu	Leu	Leu	Leu	Ser	Leu	Val	Thr	Gly	Thr
1				5					10					15	
Gln	Leu	Gly	Pro	Arg	Thr	Pro	Leu	Pro	Glu	Ala	Gly	Val	Ala	Ile	Leu
			20					25					30		
Gly	Arg	Ala	Arg	Gly	Ala	His	Arg	Pro	Gln	Pro	Arg	His	Pro	Pro	Ser
		35					40					45			
Pro	Val	Ser	Glu	Cys	Gly	Asp	Arg	Ser	Ile	Phe	Glu	Gly	Arg	Thr	Arg
	50					55					60				
Tyr	Ser	Arg	Ile	Thr	Gly	Gly	Met	Glu	Ala	Glu	Val	Gly	Glu	Phe	Pro
65					70				75						80
Trp	Gln	Val	Ser	Ile	Gln	Ala	Arg	Ser	Glu	Pro	Phe	Cys	Gly	Gly	Ser
				85					90					95	
Ile	Leu	Asn	Lys	Trp	Trp	Ile	Leu	Thr	Ala	Ala	His	Cys	Leu	Tyr	Ser
		100						105					110		
Glu	Glu	Leu	Phe	Pro	Glu	Glu	Leu	Ser	Val	Val	Leu	Gly	Thr	Asn	Asp
		115					120					125			
Leu	Thr	Ser	Pro	Ser	Met	Glu	Ile	Lys	Glu	Val	Ala	Ser	Ile	Ile	Leu
	130					135					140				
His	Lys	Asp	Phe	Lys	Arg	Ala	Asn	Met	Asp	Asn	Asp	Ile	Ala	Leu	Leu
145					150					155					160
Leu	Leu	Ala	Ser	Pro	Ile	Lys	Leu	Asp	Asp	Leu	Lys	Val	Pro	Ile	Cys
				165				170						175	
Leu	Pro	Thr	Gln	Pro	Gly	Pro	Ala	Thr	Trp	Arg	Glu	Cys	Trp	Val	Ala
			180					185					190		
Gly	Trp	Gly	Gln	Thr	Asn	Ala	Ala	Asp	Lys	Asn	Ser	Val	Lys	Thr	Asp
		195					200					205			
Leu	Met	Lys	Ala	Pro	Met	Val	Ile	Met	Asp	Trp	Glu	Glu	Cys	Ser	Lys
	210					215					220				
Met	Phe	Pro	Lys	Leu	Thr	Lys	Asn	Met	Leu	Cys	Ala	Gly	Tyr	Lys	Asn
225					230					235					240
Glu	Ser	Tyr	Asp	Ala	Cys	Lys	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys
			245					250						255	
Thr	Pro	Glu	Pro	Gly	Glu	Lys	Trp	Tyr	Gln	Val	Gly	Ile	Ile	Ser	Trp
			260					265					270		
Gly	Lys	Ser	Cys	Gly	Asp	Lys	Asn	Thr	Pro	Gly	Ile	Tyr	Thr	Ser	Leu
		275					280					285			
Val	Asn	Tyr	Asn	Leu	Trp	Ile	Glu	Lys	Val	Thr	Gln	Leu	Gly	Gly	Arg
	290					295					300				
Pro	Phe	Asn	Ala	Glu	Lys	Arg	Arg	Thr	Ser	Val	Lys	Gln	Lys	Pro	Met
305					310					315					320
Gly	Ser	Pro	Val	Ser	Gly	Val	Pro	Glu	Pro	Gly	Ser	Pro	Arg	Ser	Trp
				325					330					335	
Leu	Leu	Leu	Cys	Pro	Leu	Ser	His	Val	Leu	Phe	Arg	Ala	Ile	Leu	Tyr
			340					345					350		

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> "76A5sc2-B", an artificially synthesized primer
sequence

<400> 11

gacmacagg tgccagtcac ca	22
<210> 12	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> "SPORT SP6", an artificially synthesized primer sequence	
<400> 12	
atttaggtga cactatagaa	20
<210> 13	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> "SPORT Fw", an artificially synthesized primer sequence	
<400> 13	
tgtaaaacga cggccagt	18
<210> 14	
<211> 18	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> "Sport RV", an artificially synthesized primer sequence	
<400> 14	
caggaaacag ctatgacc	18
<210> 15	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> "No9-C", an artificially synthesized primer sequence	
<400> 15	
atgcttctgc tatcgtggaa gg	22
<210> 16	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> "SPORT T7", an artificially synthesized primer sequence	

<400> 16
 taatacgact cactataggg 20

 <210> 17
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-B", an artificially synthesized primer
 sequence

 <400> 17
 ctttgtgctg aggtcttcag tg 22

 <210> 18
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-G", an artificially synthesized primer
 sequence

 <400> 18
 cagtcaatgt cactgtggtc at 22

 <210> 19
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-J", an artificially synthesized primer
 sequence

 <400> 19
 acttgccggtt ggtgcccact tc 22

 <210> 20
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-P", an artificially synthesized primer
 sequence

 <400> 20
 gcactggaat gacaacatga tgc 23

 <210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-Q", an artificially synthesized primer
 sequence

<400> 21
 attggcgtgg caagtaggag ca 22

 <210> 22
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-N", an artificially synthesized primer
 sequence

 <400> 22
 cgagtctccc agttagcaca ga 22

 <210> 23
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-M", an artificially synthesized primer
 sequence

 <400> 23
 cggtgacttg gtcattgtctg tg 22

 <210> 24
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-K", an artificially synthesized primer
 sequence

 <400> 24
 ggatccatga aacgatggaa ggacagaag 29

 <210> 25
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-O", an artificially synthesized primer
 sequence

 <400> 25
 cgcagagttc tgctcatata ta 22

 <210> 26
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "No9-A", an artificially synthesized primer
 sequence

<400> 26
 ggcatgtagc tcactggcat g 21

 <210> 27
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "29 (-)", an artificially synthesized primer
 sequence

 <400> 27
 ggaccagcaa gaatcagttc tg 22

 <210> 28
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "17 (+) 95 (+)", an artificially synthesized
 primer sequence

 <400> 28
 ctgctaccag ttctaatttg cc 22

 <210> 29
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "G3PDH 5' ", an artificially synthesized primer
 sequence

 <400> 29
 gagattgttg ccatcaacga cc 22

 <210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "G3PDH 3' ", an artificially synthesized primer
 sequence

 <400> 30
 gttgaagtcg caggagacaa cc 22

 <210> 31
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "h-B", an artificially synthesized primer
 sequence

<400> 31
 agaggtcact gtcgagctgg g 21

 <210> 32
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "h-D", an artificially synthesized primer
 sequence

 <400> 32
 tgtgaataat gaccttctgc ac 22

 <210> 33
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "h-A", an artificially synthesized primer
 sequence

 <400> 33
 ttcagcaaca tccactcgga ga 22

 <210> 34
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "h-C", an artificially synthesized primer
 sequence

 <400> 34
 aagcaagtgc agaaggtcat ta 22

 <210> 35
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "h-F", an artificially synthesized primer
 sequence

 <400> 35
 cattggtcgt tacccactgt gc 22

 <210> 36
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "PRO1-E", an artificially synthesized primer
 sequence

<400> 36
 attctcaatg agtgggtgggt tct 23

 <210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "PRO1-D", an artificially synthesized primer
 sequence

 <400> 37
 ccagcacaca gcatattctt gg 22

 <210> 38
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "hPRO3-B", an artificially synthesized primer
 sequence

 <400> 38
 ggaaacagct cctcggaata taagc 25

 <210> 39
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "hPRO3-D", an artificially synthesized primer
 sequence

 <400> 39
 tggatgggct agttaagtcg ttggt 25

 <210> 40
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "hPRO3-A", an artificially synthesized primer
 sequence

 <400> 40
 ttcgaggggaa gaactcggta ttc 23

 <210> 41
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "hPRO3-C", an artificially synthesized primer
 sequence

<400> 41
 tgtgaaaacg gatctgatga aagcg 25

 <210> 42
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "mPRO3-B", an artificially synthesized primer
 sequence

 <400> 42
 cacctactgc caggatctgt gg 22

 <210> 43
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "mPRO3-D", an artificially synthesized primer
 sequence

 <400> 43
 ggctatatttc tcaatccaca gggta 25

 <210> 44
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "mPRO3-A", an artificially synthesized primer
 sequence

 <400> 44
 atagagtggg aggaatgctt acaga 25

 <210> 45
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> "mPRO3-C", an artificially synthesized primer
 sequence

 <400> 45
 gctacgatgc ttgccagggt g 21

 <210> 46
 <211> 12
 <212> PRT
 <213> Mus musculus

 <400> 46
 Gly Lys Cys Gln Gly Asp Ser Gly Ala Pro Met Val
 1 5 10

<210> 47
 <211> 12
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> derived from Homo sapiens and Mus musculus

 <221> VARIANT
 <222> 1
 <223> Xaa=Asp, Asn, Ser, Thr, Ala, Gly, or Cys.

 <221> VARIANT
 <222> 2
 <223> Xaa=Gly, Ser, Thr, Ala, Pro, Ile, Met, Val, Gln,
 or His.

 <221> VARIANT
 <222> 3
 <223> Xaa=any amino acid

 <221> VARIANT
 <222> 4
 <223> Xaa=any amino acid

 <221> VARIANT
 <222> 6
 <223> Xaa=Asp or Glu

 <221> VARIANT
 <222> (9)...(9)
 <223> Xaa=Gly or Ser.

 <221> VARIANT
 <222> (10)...(10)
 <223> Xaa=Ser, Ala, Pro, His, or Val.

 <221> VARIANT
 <222> (11)...(11)
 <223> Xaa=Leu, Ile, Val, Met, Phe, Tyr, Trp, or His.

 <221> VARIANT
 <222> (12)...(12)
 <223> Xaa=Leu, Ile, Val, Met, Phe, Tyr, Ser, Thr, Ala,
 Asn, Gln, or His.

 <400> 47
 Xaa Xaa Xaa Xaa Gly Xaa Ser Gly Xaa Xaa Xaa Xaa
 1 5 10

 <210> 48
 <211> 12
 <212> PRT
 <213> Homo sapiens

 <400> 48
 Gly Ile Phe Lys Gly Asp Ser Gly Ala Pro Leu Val

1 5 10

<210> 49
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> derived from Homo sapiens and Mus musculus

<221> VARIANT
<222> 1
<223> Xaa=Leu, Ile, Val, or Met.

<221> VARIANT
<222> 2
<223> Xaa=Ser or Thr.

<221> VARIANT
<222> 4
<223> Xaa=Ser, Thr, Ala, or Gly.

<400> 49
Xaa Xaa Ala Xaa His Cys
1 5

<210> 50
<211> 6
<212> PRT
<213> Mus musculus

<400> 50
Leu Thr Val Ala His Cys
1 5

<210> 51
<211> 343
<212> PRT
<213> Homo sapiens

<400> 51
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1 5 10 15
Ile Leu Leu Tyr Leu Gly Leu Leu Arg Ser Gly Thr Gly Ala Glu Gly
20 25 30
Ala Glu Ala Pro Cys Gly Val Ala Pro Gln Ala Arg Ile Thr Gly Gly
35 40 45
Ser Ser Ala Val Ala Gly Gln Trp Pro Trp Gln Val Ser Ile Thr Tyr
50 55 60
Glu Gly Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln Trp Val
65 70 75 80
Leu Ser Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu Ala Tyr
85 90 95
Glu Val Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu Asp Ala
100 105 110
Lys Val Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr Leu Gln

Thr Cys Tyr Val Thr Gly Trp Gly Tyr Ile Lys Glu Lys Ala Pro Arg
 180 185 190
 Pro Ser Pro Val Leu Met Glu Ala Arg Val Asp Leu Ile Asp Leu Asp
 195 200 205
 Leu Cys Asn Ser Thr Gln Trp Tyr Asn Gly Arg Val Thr Ser Thr Asn
 210 215 220
 Val Cys Ala Gly Tyr Pro Glu Gly Lys Ile Asp Thr Cys Gln Gly Asp
 225 230 235 240
 Ser Gly Gly Pro Leu Met Cys Arg Asp Asn Val Asp Ser Pro Phe Val
 245 250 255
 Val Val Gly Ile Thr Ser Trp Gly Val Gly Cys Ala Arg Ala Lys Arg
 260 265 270
 Pro Gly Val Tyr Thr Ala Thr Trp Asp Tyr Leu Asp Trp Ile Ala Ser
 275 280 285
 Lys Ile Gly Pro Asn Ala Leu His Leu Ile Gln Pro Ala Thr Pro His
 290 295 300
 Pro Pro Thr Thr Arg His Pro Met Val Ser Phe His Pro Pro Ser Leu
 305 310 315 320
 Arg Pro Pro Trp Tyr Phe Gln His Leu Pro Ser Arg Pro Leu Tyr Leu
 325 330 335
 Arg Pro Leu Arg Pro Leu Leu His Arg Pro Ser Ser Thr Gln Thr Ser
 340 345 350
 Ser Ser Leu Met Pro Leu Leu Ser Pro Pro Thr Pro Ala Gln Pro Ala
 355 360 365
 Ser Phe Thr Ile Ala Thr Gln His Met Arg His Arg Thr Thr Leu Ser
 370 375 380
 Phe Ala Arg Arg Leu Gln Arg Leu Ile Glu Ala Leu Lys Met Arg Thr
 385 390 395 400
 Tyr Pro Met Lys His Pro Ser Gln Tyr Ser Gly Pro Arg Asn Tyr His
 405 410 415
 Tyr Arg Phe Ser Thr Phe Glu Pro Leu Ser Asn Lys Pro Ser Glu Pro
 420 425 430
 Phe Leu His Ser
 435

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 <211> 246
 <212> PRT
 <213> Mus musculus

<400> 53
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala Phe
 1 5 10 15
 Pro Val Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Thr Cys Arg Glu
 20 25 30
 Ser Ser Val Pro Tyr Gln Val Ser Leu Asn Ala Gly Tyr His Phe Cys
 35 40 45
 Gly Gly Ser Leu Ile Asn Asp Gln Trp Val Val Ser Ala Ala His Cys
 50 55 60
 Tyr Lys Tyr Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Asn Val
 65 70 75 80
 Leu Glu Gly Asn Glu Gln Phe Val Asp Ser Ala Lys Ile Ile Arg His
 85 90 95
 Pro Asn Tyr Asn Ser Trp Thr Leu Asp Asn Asp Ile Met Leu Ile Lys
 100 105 110
 Leu Ala Ser Pro Val Thr Leu Asn Ala Arg Val Ala Ser Val Pro Leu
 115 120 125
 Pro Ser Ser Cys Ala Pro Ala Gly Thr Gln Cys Leu Ile Ser Gly Trp

130		135		140
Gly Asn Thr Leu Ser Asn Gly Val Asn Asn Pro Asp Leu Leu Gln Cys				
145		150		155
Val Asp Ala Pro Val Leu Pro Gln Ala Asp Cys Glu Ala Ser Tyr Pro				160
		165		170
Gly Asp Ile Thr Asn Asn Met Ile Cys Val Gly Phe Leu Glu Gly Gly				175
		180		185
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly				190
		195		200
Glu Leu Gln Gly Ile Val Ser Trp Gly Tyr Gly Cys Ala Gln Pro Asp				205
		210		215
Ala Pro Gly Val Tyr Thr Lys Val Cys Asn Tyr Val Asp Trp Ile Gln				220
225		230		235
Asn Thr Ile Ala Asp Asn				240
		245		